

# SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Eaton, Dan L.  
de Sauvage, Frederic J.

(ii) TITLE OF INVENTION: MPL LIGAND

10 (iii) NUMBER OF SEOUENCES: 21

(iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Genentech, Inc.  
(B) STREET: 460 Point San Bruno Blvd  
(C) CITY: South San Francisco  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94080

20 (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/430035  
(B) FILING DATE: 27-Apr-1995  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/196689  
(B) FILING DATE: 15-FEB-1994

35 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/185607  
(B) FILING DATE: 21-JAN-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/176553  
(B) FILING DATE: 03-JAN-1994

(viii) ATTORNEY/AGENT INFORMATION:

45 (A) NAME: Winter, Daryl B.  
(B) REGISTRATION NUMBER: 32,637  
(C) REFERENCE/DOCKET NUMBER: P0871P2D2

(ix) TELECOMMUNICATION INFORMATION:

50 (A) TELEPHONE: 415/225-1249  
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(C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

10 Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu  
-16 -15 -10 -5  
Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys  
1 5 10  
15 Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu  
15 20 25 26

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

B' 30 GAATTCCTGG AATACCAGCT GACAATGATT TCCTCCTCAT CTTTCAACCT 50  
cont. CACCTCTCCT CATCTAAGAA TTG CTC CTC GTG GTC ATG CTT 91  
Leu Leu Leu Val Val Met Leu  
-16 -15 -10  
35 CTC CTA ACT GCA AGG CTA ACG CTG TCC AGC CCG GCT CCT 130  
Leu Leu Thr Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro  
-5 1  
40 CCT GCT TGT GAC CTC CGA GTC CTC AGT AAA CTG CTT CGT 169  
Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg  
5 10 15  
45 GAC TCC CAT GTC CTT CAC AGC AGA CTG GTGA GAACTCCCAA 210  
Asp Ser His Val Leu His Ser Arg Leu  
20 25 26  
CATTATCCCC TTTATCCGCG TAACTGGTAA GACACCCATA CTCCCAGGAA 260  
50 GACACCATCA CTTCTCTAA CTCCTTGACC CAATGACTAT TCTTCCCATA 310  
TTGTCCCCAC CTA CTGATCA CACTCTCTGA CAAGAATTAT TCTTCACAAT 360

ACAGCCCGCA TTTAAAAGCT CTCGTCTAGA 390

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 390 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCTAGACGAG AGCTTTTAAA TGCGGGCTGT ATTGTGAAGA ATAATTCTTG 50  
TCAGAGAGTG TGATCAGTAG GTGGGGACAA TATGGGAAGA ATAGTCATTG 100  
GGTCAAGGAG TTAGAGGAAG TGATGGTGTC TTCCTGGGAG TATGGGTGTC 150  
TTACCAGTTA CGCGGATAAA GGGGATAATG TTGGGAGTTC TCACCAGTCT 200  
GCTGTGAAGG ACATGGGAGT CACGAAGCAG TTTACTGAGG ACTCGGAGGT 250  
CACAAGCAGG AGGAGCCGGG CTGGACAGCG TTAGCCTTGC AGTTAGGAGA 300  
AGCATGACCA CGAGGAGCAA TTCTTAGATG AGGAGAGGTG AGGTTGAAAG 350  
ATGAGGAGGA AATCATTGTC AGCTGGTATT CCAGGAATTC 390

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 353 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr  
-21 -20 -15 -10  
Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu  
-5 1 5  
Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser  
10 15 20  
Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val  
25 30 35  
Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln  
40 45 50

	Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	
	55					60					65					
5	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	
	70					75					80					
	Cys	Leu	Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	
	85					90					95					
10	Leu	Leu	Gly	Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Leu	Pro	Pro	
	100					105					110					
	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	Leu	
	115					120					125					
15	Ser	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	
	130					135					140					
	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Arg	Ala	Pro	Pro	Thr	Thr	
20	145					150					155					
	Ala	Val	Pro	Ser	Arg	Thr	Ser	Leu	Val	Leu	Thr	Leu	Asn	Glu	Leu	
	160					165					170					
25	Pro	Asn	Arg	Thr	Ser	Gly	Leu	Leu	Glu	Thr	Asn	Phe	Thr	Ala	Ser	
	175					180					185					
	Ala	Arg	Thr	Thr	Gly	Ser	Gly	Leu	Leu	Lys	Trp	Gln	Gln	Gly	Phe	
	190					195					200					
30	Arg	Ala	Lys	Ile	Pro	Gly	Leu	Leu	Asn	Gln	Thr	Ser	Arg	Ser	Leu	
	205					210					215					
	Asp	Gln	Ile	Pro	Gly	Tyr	Leu	Asn	Arg	Ile	His	Glu	Leu	Leu	Asn	
35	220					225					230					
	Gly	Thr	Arg	Gly	Leu	Phe	Pro	Gly	Pro	Ser	Arg	Arg	Thr	Leu	Gly	
	235					240					245					
40	Ala	Pro	Asp	Ile	Ser	Ser	Gly	Thr	Ser	Asp	Thr	Gly	Ser	Leu	Pro	
	250					255					260					
	Pro	Asn	Leu	Gln	Pro	Gly	Tyr	Ser	Pro	Ser	Pro	Thr	His	Pro	Pro	
	265					270					275					
45	Thr	Gly	Gln	Tyr	Thr	Leu	Phe	Pro	Leu	Pro	Pro	Thr	Leu	Pro	Thr	
	280					285					290					
	Pro	Val	Val	Gln	Leu	His	Pro	Leu	Leu	Pro	Asp	Pro	Ser	Ala	Pro	
50	295					300					305					

Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His  
310 315 320

5 Ser Gln Asn Leu Ser Gln Glu Gly  
325 330 332

(2) INFORMATION FOR SEQ ID NO:5:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1798 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCGTCTTCCT ACCCATCTGC TCCCCAGAGG GCTGCCTGCT GTGCACTTGG 50

20 GTCCTGGAGC CCTTCTCCAC CCGGATAGAT TCCTCACCCCT TGGCCCGCCT 100

TTGCCCCACC CTACTCTGCC CAGAAGTGCA AGAGCCTAAG CCGCCTCCAT 150

25 GGCCCCAGGA AGGATTCAGG GGAGAGGCC CAAACAGGGA GCCACGCCAG 200

CCAGACACCC CGGCCAGA ATG GAG CTG ACT GAA TTG CTC CTC 242  
Met Glu Leu Thr Glu Leu Leu Leu  
-21 -20 -15

30 GTG GTC ATG CTT CTC CTA ACT GCA AGG CTA ACG CTG TCC 281  
Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu Ser  
-10 -5

35 AGC CCG GCT CCT CCT GCT TGT GAC CTC CGA GTC CTC AGT 320  
Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser  
1 5 10

40 AAA CTG CTT CGT GAC TCC CAT GTC CTT CAC AGC AGA CTG 359  
Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu  
15 20 25

45 AGC CAG TGC CCA GAG GTT CAC CCT TTG CCT ACA CCT GTC 398  
Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val  
30 35

CTG CTG CCT GCT GTG GAC TTT AGC TTG GGA GAA TGG AAA 437  
Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys  
40 45 50

50 ACC CAG ATG GAG GAG ACC AAG GCA CAG GAC ATT CTG GGA 476  
Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly  
55 60 65

	GCA	GTG	ACC	CTT	CTG	CTG	GAG	GGA	GTG	ATG	GCA	GCA	CGG	515
	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	
					70					75				
5	GGA	CAA	CTG	GGA	CCC	ACT	TGC	CTC	TCA	TCC	CTC	CTG	GGG	554
	Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu	Gly	
		80					85					90		
10	CAG	CTT	TCT	GGA	CAG	GTC	CGT	CTC	CTC	CTT	GGG	GCC	CTG	593
	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	
				95					100					
15	CAG	AGC	CTC	CTT	GGA	ACC	CAG	CTT	CCT	CCA	CAG	GGC	AGG	632
	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Leu	Pro	Pro	Gln	Gly	Arg	
	105					110					115			
20	ACC	ACA	GCT	CAC	AAG	GAT	CCC	AAT	GCC	ATC	TTC	CTG	AGC	671
	Thr	Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	Leu	Ser	
			120					125					130	
25	TTC	CAA	CAC	CTG	CTC	CGA	GGA	AAG	GTG	CGT	TTC	CTG	ATG	710
	Phe	Gln	His	Leu	Leu	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	
					135					140				
30	CTT	GTA	GGA	GGG	TCC	ACC	CTC	TGC	GTC	AGG	CGG	GCC	CCA	749
	Leu	Val	Gly	Gly	Ser	Thr	Leu	Cys	Val	Arg	Arg	Ala	Pro	
		145					150					155		
35	CCC	ACC	ACA	GCT	GTC	CCC	AGC	AGA	ACC	TCT	CTA	GTC	CTC	788
	Pro	Thr	Thr	Ala	Val	Pro	Ser	Arg	Thr	Ser	Leu	Val	Leu	
				160					165					
40	ACA	CTG	AAC	GAG	CTC	CCA	AAC	AGG	ACT	TCT	GGA	TTG	TTG	827
	Thr	Leu	Asn	Glu	Leu	Pro	Asn	Arg	Thr	Ser	Gly	Leu	Leu	
	170					175					180			
45	GAG	ACA	AAC	TTC	ACT	GCC	TCA	GCC	AGA	ACT	ACT	GGC	TCT	866
	Glu	Thr	Asn	Phe	Thr	Ala	Ser	Ala	Arg	Thr	Thr	Gly	Ser	
			185					190					195	
50	GGG	CTT	CTG	AAG	TGG	CAG	CAG	GGA	TTC	AGA	GCC	AAG	ATT	905
	Gly	Leu	Leu	Lys	Trp	Gln	Gln	Gly	Phe	Arg	Ala	Lys	Ile	
				200						205				
55	CCT	GGT	CTG	CTG	AAC	CAA	ACC	TCC	AGG	TCC	CTG	GAC	CAA	944
	Pro	Gly	Leu	Leu	Asn	Gln	Thr	Ser	Arg	Ser	Leu	Asp	Gln	
		210					215					220		
60	ATC	CCC	GGA	TAC	CTG	AAC	AGG	ATA	CAC	GAA	CTC	TTG	AAT	983
	Ile	Pro	Gly	Tyr	Leu	Asn	Arg	Ile	His	Glu	Leu	Leu	Asn	
				225					230					

GGA ACT CGT GGA CTC TTT CCT GGA CCC TCA CGC AGG ACC 1022  
 Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr  
 235 240 245

5 CTA GGA GCC CCG GAC ATT TCC TCA GGA ACA TCA GAC ACA 1061  
 Leu Gly Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr  
 250 255 260

10 GGC TCC CTG CCA CCC AAC CTC CAG CCT GGA TAT TCT CCT 1100  
 Gly Ser Leu Pro Pro Asn Leu Gln Pro Gly Tyr Ser Pro  
 265 270

15 TCC CCA ACC CAT CCT CCT ACT GGA CAG TAT ACG CTC TTC 1139  
 Ser Pro Thr His Pro Pro Thr Gly Gln Tyr Thr Leu Phe  
 275 280 285

20 CCT CTT CCA CCC ACC TTG CCC ACC CCT GTG GTC CAG CTC 1178  
 Pro Leu Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu  
 290 295

CAC CCC CTG CTT CCT GAC CCT TCT GCT CCA ACG CCC ACC 1217  
 His Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr  
 300 305 310

25 CCT ACC AGC CCT CTT CTA AAC ACA TCC TAC ACC CAC TCC 1256  
 Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His Ser  
 315 320 325

*B' 30*  
*cont.* CAG AAT CTG TCT CAG GAA GGG TAA GGTTCCTCAGA CACTGCCGAC 1300  
 Gln Asn Leu Ser Gln Glu Gly  
 330 332

ATCAGCATTG TCTCATGTAC AGCTCCCTTC CCTGCAGGGC GCCCCTGGGA 1350

35 GACAACTGGA CAAGATTTCC TACTTTCTCC TGAAACCCAA AGCCCTGGTA 1400

AAAGGGATAC ACAGGACTGA AAAGGGAATC ATTTTTCACCT GTACATTATA 1450

40 AACCTTCAGA AGCTATTTTT TTAAGCTATC AGCAATACTC ATCAGAGCAG 1500

CTAGCTCTTT GGTCTATTTT CTGCAGAAAT TTGCAACTCA CTGATTCTCT 1550

ACATGCTCTT TTTCTGTGAT AACTCTGCAA AGGCCTGGGC TGGCCTGGCA 1600

45 GTTGAACAGA GGGAGAGACT AACCTTGAGT CAGAAAACAG AGAAAGGGTA 1650

ATTCCTTTTG CTTCAAATTC AAGGCCTTCC AACGCCCCCA TCCCCTTTAC 1700

50 TATCATTCTC AGTGGGACTC TGATCCATA TTCTTAACAG ATCTTTACTC 1750

TTGAGAAATG AATAAGCTTT CTCTCAGAAA AAAAAAAAAA AAAAAAAAAA 1798

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1798 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTTTTTTTT TTTTTTTTTT TCTGAGAGAA AGCTTATTCA TTTCTCAAGA 50  
GTAAAGATCT GTTAAGAATA TGGGATCAGA GTCCCACTGA GAATGATAGT 100  
AAAGGGGATG GGGGCGTTGG AAGGCCTTGA ATTTGAAGCA AAGGAAATTA 150  
CCCTTTCTCT GTTTTCTGAC TCAAGGTTAG TCTCTCCCTC TGTTCAACTG 200  
CCAGGCCAGC CCAGGCCTTT GCAGAGTTAT CACAGAAAAA GAGCATGTAG 250  
AGAATCAGTG AGTTGCAAAT TTCTGCAGAA AATAGACCAA AGAGCTAGCT 300  
GCTCTGATGA GTATTGCTGA TAGCTTAAAA AAATAGCTTC TGAAGGTTTA 350  
TAATGTACAG TGAAAAATGA TTCCCTTTTC AGTCCTGTGT ATCCCTTTTA 400  
CCAGGGCTTT GGGTTTCAGG AGAAAGTAGG AAATCTTGTC CAGTTGTCTC 450  
CCAGGGGCGC CCTGCAGGGA AGGGAGCTGT ACATGAGACA ATGCTGATGT 500  
CGGCAGTGTC TGAGAACCTT ACCCTTCCTG AGACAGATTC TGGGAGTGGG 550  
TGTAGGATGT GTTTAGAAGA GGGCTGGTAG GGGTGGGCGT TGGAGCAGAA 600  
GGGTCAGGAA GCAGGGGGTG GAGCTGGACC ACAGGGGTGG GCAAGGTGGG 650  
TGGAAGAGGG AAGAGCGTAT ACTGTCCAGT AGGAGGATGG GTTGGGGAAG 700  
GAGAATATCC AGGCTGGAGG TTGGGTGGCA GGGAGCCTGT GTCTGATGTT 750  
CCTGAGGAAA TGTCCGGGGC TCCTAGGGTC CTGCGTGAGG GTCCAGGAAA 800  
GAGTCCACGA GTTCCATTCA AGAGTTCGTG TATCCTGTTC AGGTATCCGG 850  
GGATTTGGTC CAGGGACCTG GAGGTTTGGT TCAGCAGACC AGGAATCTTG 900  
GCTCTGAATC CCTGCTGCCA CTTCAGAAGC CCAGAGCCAG TAGTTCTGGC 950  
TGAGGCAGTG AAGTTTGTCT CCAACAATCC AGAAGTCCTG TTTGGGAGCT 1000  
CGTTCAGTGT GAGGACTAGA GAGGTTCTGC TGGGGACAGC TGTGGTGGGT 1050



GGGGCCCCGCC TGACGCAGAG GGTGGACCCT CCTACAAGCA TCAGGAAACG 1100  
 CACCTTTCCT CGGAGCAGGT GTTGAAGCT CAGGAAGATG GCATTGGGAT 1150  
 5 CCTTGTGAGC TGTGGTCCTG CCCTGTGGAG GAAGCTGGGT TCCAAGGAGG 1200  
 CTCTGCAGGG CCCCAAGGAG GAGACGGACC TGTCCAGAAA GCTGCCCCAG 1250  
 10 GAGGGATGAG AGGCAAGTGG GTCCCAAGTTG TCCCCGTGCT GCCATCACTC 1300  
 CCTCCAGCAG AAGGGTCACT GCTCCCAGAA TGTCTGTGC CTTGGTCTCC 1350  
 TCCATCTGGG TTTTCCATTC TCCCAAGCTA AAGTCCACAG CAGGCAGCAG 1400  
 15 GACAGGTGTA GGCAAAGGGT GAACCTCTGG GCACTGGCTC AGTCTGCTGT 1450  
 GAAGGACATG GGAGTCACGA AGCAGTTTAC TGAGGACTCG GAGGTCACAA 1500  
 GCAGGAGGAG CCGGGCTGGA CAGCGTTAGC CTTGCAGTTA GGAGAAGCAT 1550  
 20 GACCACGAGG AGCAATTCAG TCAGCTCCAT TCTGGCCGGG GTGTCTGGCT 1600  
 GGCGTGGCTC CCTGTTTGGG GCCTCTCCCC TGAATCCTTC CTGGGGCCAT 1650  
 25 GGAGGCGGCT TAGGCTCTTG CACTTCTGGG CAGAGTAGGG TGGGGCAAAG 1700  
 GCGGGCCAAG GGTGAGGAAT CTATCCGGGT GGAGAAGGGC TCCAGGACCC 1750  
 AAGTGCACAG CAGGCAGCCC TCTGGGGAGC AGATGGGTAG GAAGACGC 1798

*B' 30*  
*cont.*  
(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

40 Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser  
     1                    5                    10                    15  
 Leu Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro  
                     20                    25                    30  
 45 Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu  
                     35                    40                    45  
 Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys  
 50                    50                    55                    60

Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe  
 65 70 75  
 Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val  
 5 80 85 90  
 Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln  
 95 100 105  
 Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu  
 10 110 115 120  
 His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu  
 125 130 135  
 15 Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp  
 140 145 150  
 Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe  
 20 155 160 165  
 Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu  
 170 175 180  
 25 Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg  
 185 190 193

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu  
 1 5 10 15  
 Leu Arg Asp Asp His Val Leu His Gly Arg  
 20 25

(2) INFORMATION FOR SEQ ID NO:9:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 26 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu  
1 5 10 15

Leu Arg Asp Ser His Val Leu His Ser Arg Leu  
20 25 26

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu  
1 5 10 15

Leu Arg Asp Asp Xaa Val Leu His Gly Arg Leu  
20 25 26

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ser Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Leu Asn Lys Leu  
1 5 10 15

Leu Arg Asp Asp His Val Leu His Gly Arg  
20 25

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Xaa Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Xaa Asn Lys  
1 5 10 14

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs

(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCCGTGAAGG ACGTGGTCGT CACGAAGCAG TTTATTTAGG AGTCG 45

10 (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs  
(B) TYPE: Nucleic Acid  
15 (C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

20

CCNGCNCNC CNGCNTGYGA 20

(2) INFORMATION FOR SEQ ID NO:15:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

NCCRTGNARN ACRTGRTCRT C 21

35

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 base pairs  
40 (B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

45

CCAGCGCCGC CAGCCTGTGA CCCCCGACTC CTAAATAAAC TGCCTCGTGA 50

TGACCACGTT CAGCACGGC 69

50

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCAGCACCTC CGGCATGTGA CCCCCGACTC CTAAATAAAC TGCTTCGTGA 50  
CGACCACGTC CATCACGGC 69

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Pro Arg Leu Leu Asn Lys Leu Leu Arg  
1 5 9

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCAGCACCGC CGGCATGTGA CCCCCGACTC CTAAATAAAC TGCTTCGTGA 50  
CGATCATGTC TATCACGGT 69

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCTAGCTCTA GAAATTGCTC CTCGTGGTCA TGCTTCT 37

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CAGTCTGCCG TGAAGGACAT GG 22

B'  
overl.